



#3

# SEQUENCE LISTING

<110> Bowen, Benjamin A.  
Deakin, Edward  
Goldsmith, Neil  
Haudenschild, Christian  
Houck, David  
McAlpine, James B.  
Neilsen, Soren  
Pazoles, Christopher  
Spencer, Marget E.  
Stafford, Angela

<120> Methods for Identifying Genes Regulating  
Desired Cell Phenotypes

<130> 50273/005002

<140> US 10/056,479

<141> 2002-01-24

<150> US 60/263,807

<151> 2001-01-24

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1

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His	Gly	Gly	Asn	Phe	Gln	Gly	Thr	Pro	Ile	Gly	Val	Ser	Met	Asp	Asn
			20					25					30		
Thr	Arg	Leu	Ala	Leu	Ala	Ala	Ile	Gly	Lys	Leu	Met	Phe	Ala	Gln	Phe
		35					40					45			
Ser	Glu	Leu	Val	Asn	Asp	Phe	Tyr	Asn	Asn	Gly	Leu	Pro	Ser	Asn	Leu
	50					55					60				
Ser	Gly	Ser	Arg	Asn	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Lys	Gly	Ala	Glu
65				70					75					80	
Ile	Ala	Met	Ala	Ser	Tyr	Cys	Ser	Glu	Leu	Gln	Phe	Leu	Gly	Asn	Pro
				85				90						95	
Val	Thr	Asn	His	Val	Gln	Ser	Ala	Glu	Gln	His	Asn	Gln	Asp	Val	Asn
		100					105						110		
Ser	Leu	Gly	Leu	Ile	Ser	Ser	Arg	Lys	Thr	Ala	Glu	Ala	Val	Asp	Ile
		115					120					125			
Leu	Lys	Leu	Met	Thr	Ser	Thr	Tyr	Leu	Val	Ala	Leu	Cys	Gln	Ala	Val
	130					135					140				
Asp	Leu	Arg	His	Met	Glu	Glu	Asn	Leu	Arg	Asn	Thr	Val	Lys	Asn	Thr
145					150				155						160

Val Ser Gln Val Ala Lys Arg Thr Leu Thr Thr Gly Ala Asn Gly Glu  
165 170 175  
Leu His Pro Ser Arg Phe Cys Glu Lys Asp Leu Leu Lys Val Val Asp  
180 185 190  
Arg Glu Tyr Val Phe Ala Tyr Ile Asp Asp Pro Cys Leu Ala Thr Tyr  
195 200 205  
Pro Leu Met Gln Ser Leu Gly Ala  
210 215

<210> 2  
<211> 648  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

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ttccaaggaa ccccgatcgg tgtgtccatg gacaacacca ggctagcact ggcagctatt 120  
gggaagctca tgtttgctca gttctccgag cttgtcaatg acttctacaa caatggctctg 180  
ccatcgaatc tgtctggcag caggaacccc agcttgact atgggcttaa aggagcggag 240  
atcgcaatgg cttcctactg ttccgarctt cagttccttg gtaaccgggt tactaaccat 300  
gtccagagcg ctgagcagca taaccaggat gtcaactcat tgggattgat ctcatcaagg 360  
aagacagctg aagctgttga catcttgaag ctcatgacat cgacttactt ggtggccctt 420  
tgccaagctg ttgacctgag gcacatggaa gagaatctta ggaacactgt gaagaacacc 480  
gtgagccaag tcgccaagag gacgctcaac acaggagcca acggtgagct tcacccatcg 540  
agattctgcg agaaggactt gctcaaagtr gttgacagag agtatgtgtt cgcgtacatt 600  
gatgaccctt gcttggaac ttaccctctg atgcaaagct taggggct 648

<210> 3  
<211> 117  
<212> PRT  
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<220>  
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Glu Asn Asn Lys Gly Ala Arg Val Leu Val Ile Cys Ser Glu Ile Thr  
1 5 10 15  
Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Tyr Ser Leu Val  
20 25 30  
Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Val Ile Leu Gly Ala  
35 40 45  
Asp Pro Leu Pro Glu Glu Lys Pro Met Phe Glu Leu Val Ser Ala Ala  
50 55 60  
Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Asp Gly His Leu Ser  
65 70 75 80  
Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro Gly Leu Ile  
85 90 95  
Ser Lys Asn Ile Glu Lys Gly Leu Val Glu Ala Phe Lys Pro Ile Gly  
100 105 110  
Ile Glu Asp Gly Thr  
115

<210> 4

<211> 353  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> misc\_feature  
 <222> 183  
 <223> n = A,T,C or G

<223> Synthetic

<400> 4  
 gagaacaaca agggcgctcg cgtgttggtg atttgctctg agatcactgc tgttaccttc 60  
 cgtggcccaa gcgatactca tttgtacagt cttgtaggtc aggccttggt cggagacgga 120  
 gctgcagcag tcatcctcgg agcagacccc cttcccgaag agaagcccat gtttgaactt 180  
 gtntctgcag ctcagaccat cttgccagac agtgaaggcg ccatcgacgg tcattcttagt 240  
 gaagttggtc tcacattcca tttgcttaag gacgttcccc ggctgatctc caagaacatt 300  
 gagaagggtc tagtcgaggc attcaagcct atcggtatcg aagacggaac tca 353

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<220>  
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<223> Synthetic

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 Pro Glu Ala Val Lys Asp Trp Arg Glu Ile Val Thr Tyr Phe Ser Tyr  
 1 5 10 15  
 Pro Val Ser Ala Arg Asp Tyr Ser Arg Trp Pro Asp Lys Pro Glu Ala  
 20 25 30  
 Trp Lys Glu Val Thr Lys Arg Tyr Ser Asp Thr Leu Met Gly Leu Ala  
 35 40 45  
 Cys Lys Leu Xaa Glu Val Leu Ser Glu Ala Met Gly Leu Glu Lys Glu  
 50 55 60  
 Ala Leu Thr Lys Ala Cys Val Asp Met Asp Gln Lys Val Val Val Asn  
 65 70 75 80  
 Tyr Tyr Pro Lys Cys Pro Glu Pro Asp Leu Thr Leu Gly Leu Lys Arg  
 85 90 95  
 His Thr Asp Pro Gly Thr Ile Thr Leu Leu Gln Asp Gln Val Gly  
 100 105 110  
 Gly Leu Gln Ala Thr Arg Asp Asp Gly Lys  
 115 120

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 <212> DNA  
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<220>  
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<400> 6

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agcgacacgc tgatgggtct ggcatgtaag cttstaggagg tcttatctga agcgatggga 180
ctagagaagg aggtcttgac taaggcctgt gttgacatgg accagaaagt tgttgtcaac 240
tactacccca agtgtcctga gcctgatcta actttggggac tcaagaggca taccgacccc 300
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ggtaagac

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<210> 7
<211> 23
<212> DNA
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<220>
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<400> 7
gartayaayc cvaagcgttt tgc

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23

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<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 8
ggrtakatgt tytcraaggc rg

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22

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<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 9
atgatgtacc arcarggggtg cttygc

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26

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<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 10
agcccgggaa cgtccttaag c

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21

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<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 11 gtsaacgaca accckttgat cgatg	25
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<400> 12 acttggctca csgtggttctt sac	23
<210> 13 <211> 24 <212> DNA <213> Artificial Sequence	
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<400> 13 gaaggaggtg accaagcggtt acag	24
<210> 14 <211> 25 <212> DNA <213> Artificial Sequence	
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<400> 14 tggcctgaag cccgccaaact tggtc	25
<210> 15 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Synthetic	
<400> 15 tttttttttt tttttttt	18